

Exhibit A

BLAST**Basic Local Alignment Search Tool**

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Blast 2 sequences

SEQ ID NO:1 vs. XM_044533Results for: ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|46661

lcl|46661

Description

None

Molecule type

amino acid

Query Length

837

Subject ID

46663

Description

None

Molecule type

amino acid

Subject Length

837

ProgramBLASTP 2.2.23+ [Citation](#)Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Multiple alignment](#)]

[Search Parameters](#)**Search parameter name Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1

Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.320342	0.267
K	0.136493	0.041
H	0.42551	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

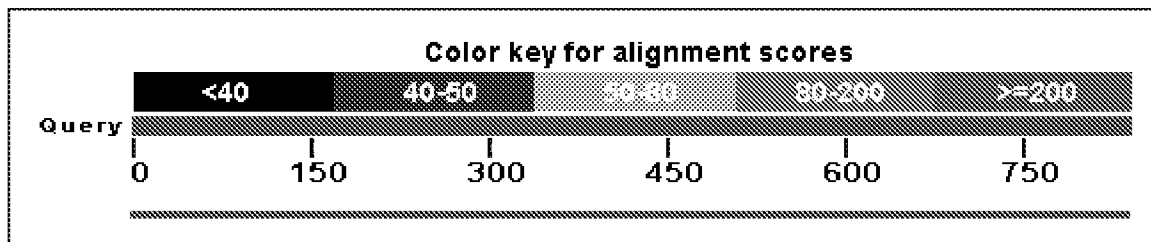
Effective search space	632025
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Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#)

Plot of lcl|46661 vs 46663 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
46663	unnamed protein product	1698	1698	100%	0.0	

Alignments

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)

>lcl|46663 unnamed protein product
Length=837

Score = 1698 bits (4398), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 831/837 (99%), Positives = 831/837 (99%), Gaps = 0/837 (0%)

Query	1	MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFL	60
Sbjct	1	MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFL	60
Query	61	RFEAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQC	120
Sbjct	61	RFEAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQC	120
Query	121	SFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLED	180
Sbjct	121	SFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLED	180
Query	181	GKGRCFPDPNFKSTALVVDGELYTGTVSSFGQNDPAISRSQSLRPTKTESSLNWLQDPAF	240
Sbjct	181	GKGRCFPDPNFKSTALVVDGELYTGTVSSFGQNDPAISRSQSLRPTKTESSLNWLQDPAF	240
Query	241	VASAYIPESLGSQGGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRW	300
Sbjct	241	VASAYIPESLGSQGGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRW	300
Query	301	TSFLKAQLLCSRPDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCV	360
Sbjct	301	TSFLKAQLLCSRPDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCV	360
Query	361	FTMKDVQRVFSGLYKEVNRETQQMVHRDPPVPTPRPGACITNSARERKINSSLQLPDRVL	420
Sbjct	361	FTMKDVQRVFSGLYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVL	420

Query	421	NFLKDHFLMDGQVRSRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVG	480
Sbjct	421	NFLKDHFLMDGQVRSRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVG	480
Query	481	PRVHIIIEELQIFSSGQPVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARD	540
Sbjct	481	PRVHIIIEELQIFSSGQPVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARD	540
Query	541	PYCAWSGSSCKHVSLEYQPLATRPWIQDIEGASAKDLCSSASSVSPSFVPTGEKPCEQVQ	600
Sbjct	541	PYCAWSGSSCKHVSLEYQPLATRPWIQDIEGASAKDLCSSASSVSPSFVPTGEKPCEQVQ	600
Query	601	FQPNTVNTLACPLLSNLATRLWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLE	660
Sbjct	601	FQPNTVNTLACPLLSNLATRLWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLE	660
Query	661	EGFQQQLVASYCPEVVEDGVADQTDGGSVPVPIISTSRVSAPAGGKASWGADRSYWKEFLV	720
Sbjct	661	EGFQQQLVASYCPEVVEDGVADQTDGGSVPVPIISTSRVSAPAGGKASWGADRSYWKEFLV	720
Query	721	MCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAVHPKTCPVVLPPEPTRPLNGLGPPST	780
Sbjct	721	MCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAVHPKTCPVVLPPEPTRPLNGLGPPST	780
Query	781	PLDHRGYQSLSDSPPGSRVFTSEKRPLSIQDSFVEVSPVCPRPVRLGSEIRDSVV	837
Sbjct	781	PLDHRGYQSLSDSPPGSRVFTSEKRPLSIQDSFVEVSPVCPRPVRLGSEIRDSVV	837

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)